SEQUENCE LISTING

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Demo, Susan
Jenkins, Yonchu
Rigel Pharmaceuticals, Inc.

<120> MRE11: Modulation of Cellular Proliferation

<130> 021044-001310US

<140> US 10/026,331
<141> 2001-12-21

<150> US 60/309,737
<151> 2001-08-01

<160> 21

<170> PatentIn Ver. 2.1

<210> 1
<211> 2537
<212> DNA
<213> Homo sapiens

<220>
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<222> (171)..(2297)
<223> MRE11

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<210> 2
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<213> Homo sapiens

<220>
<223> human MRE11 meiotic recombination 11 homolog A

<400> 2

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Gly Asn Asp Thr Phe Val Thr Leu Asp Glu Ile Leu Arg Leu Ala Gln
        35                  40                  45
Glu Asn Glu Val Asp Phe Ile Leu Leu Gly Gly Asp Leu Phe His Glu
    50                  55                  60
Asn Lys Pro Ser Arg Lys Thr Leu His Thr Cys Leu Glu Leu Leu Arg
65                  70                  75                  80
Lys Tyr Cys Met Gly Asp Arg Pro Val Gln Phe Glu Ile Leu Ser Asp
                85                  90                  95
Gln Ser Val Asn Phe Gly Phe Ser Lys Phe Pro Trp Val Asn Tyr Gln
            100                 105                 110
Asp Gly Asn Leu Asn Ile Ser Ile Pro Val Phe Ser Ile His Gly Asn
        115                 120                 125
His Asp Asp Pro Thr Gly Ala Asp Ala Leu Cys Ala Leu Asp Ile Leu
    130                 135                 140
Ser Cys Ala Gly Phe Val Asn His Phe Gly Arg Ser Met Ser Val Glu
145                 150                 155                 160
Lys Ile Asp Ile Ser Pro Val Leu Leu Gln Lys Gly Ser Thr Lys Ile
                165                 170                 175
Ala Leu Tyr Gly Leu Gly Ser Ile Pro Asp Glu Arg Leu Tyr Arg Met
            180                 185                 190
Phe Val Asn Lys Lys Val Thr Met Leu Arg Pro Lys Glu Asp Glu Asn
        195                 200                 205
Ser Trp Phe Asn Leu Phe Val Ile His Gln Asn Arg Ser Lys His Gly
    210                 215                 220
Ser Thr Asn Phe Ile Pro Glu Gln Phe Leu Asp Asp Phe Ile Asp Leu
225                 230                 235                 240
Val Ile Trp Gly His Glu His Glu Cys Lys Ile Ala Pro Thr Lys Asn
                245                 250                 255
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Glu Gln Gln Leu Phe Tyr Ile Ser Gln Pro Gly Ser Ser Val Val Thr
260 265 270
Ser Leu Ser Pro Gly Glu Ala Val Lys Lys His Val Gly Leu Leu Arg
275 280 285
Ile Lys Gly Arg Lys Met Asn Met His Lys Ile Pro Leu His Thr Val
290 295 300
Arg Gln Phe Phe Met Glu Asp Ile Val Leu Ala Asn His Pro Asp Ile
305 310 315 320
Phe Asn Pro Asp Asn Pro Lys Val Thr Gln Ala Ile Gln Ser Phe Cys
325 330 335
Leu Glu Lys Ile Glu Glu Met Leu Glu Asn Ala Glu Arg Glu Arg Leu
340 345 350
Gly Asn Ser His Gln Pro Glu Lys Pro Leu Val Arg Leu Arg Val Asp
355 360 365
Tyr Ser Gly Gly Phe Glu Pro Phe Ser Val Leu Arg Phe Ser Gln Lys
370 375 380
Phe Val Asp Arg Val Ala Asn Pro Lys Asp Ile Ile His Phe Phe Arg
385 390 395 400
His Arg Glu Gln Lys Glu Lys Thr Gly Glu Glu Ile Asn Phe Gly Lys
405 410 415
Leu Ile Thr Lys Pro Ser Glu Gly Thr Thr Leu Arg Val Glu Asp Leu
420 425 430
Val Lys Gln Tyr Phe Gln Thr Ala Glu Lys Asn Val Gln Leu Ser Leu
435 440 445
Leu Thr Glu Arg Gly Met Gly Glu Ala Val Gln Glu Phe Val Asp Lys
450 455 460
Glu Glu Lys Asp Ala Ile Glu Glu Leu Val Lys Tyr Gln Leu Glu Lys
465 470 475 480
Thr Gln Arg Phe Leu Lys Glu Arg His Ile Asp Ala Leu Glu Asp Lys
485 490 495
Ile Asp Glu Glu Val Arg Arg Phe Arg Glu Thr Arg Gln Lys Asn Thr
500 505 510
Asn Glu Glu Asp Asp Glu Val Arg Glu Ala Met Thr Arg Ala Arg Ala
515 520 525
Leu Arg Ser Gln Ser Glu Glu Ser Ala Ser Ala Phe Ser Ala Asp Asp
530 535 540
Leu Met Ser Ile Asp Leu Ala Glu Gln Met Ala Asn Asp Ser Asp Asp
545 550 555 560
Ser Ile Ser Ala Ala Thr Asn Lys Gly Arg Gly Arg Gly Arg Gly Arg
565 570 575
Arg Gly Gly Arg Gly Gln Asn Ser Ala Ser Arg Gly Gly Ser Gln Arg
580 585 590
Gly Arg Ala Asp Thr Gly Leu Glu Thr Ser Thr Arg Ser Arg Asn Ser
595 600 605
Lys Thr Ala Val Ser Ala Ser Arg Asn Met Ser Ile Ile Asp Ala Phe
610 615 620
Lys Ser Thr Arg Gln Gln Pro Ser Arg Asn Val Thr Thr Lys Asn Tyr
625 630 635 640
Ser Glu Val Ile Glu Val Asp Glu Ser Asp Val Glu Glu Asp Ile Phe
645 650 655
Pro Thr Thr Ser Lys Thr Asp Gln Arg Trp Ser Ser Thr Ser Ser Ser
660 665 670
Lys Ile Met Ser Gln Ser Gln Val Ser Lys Gly Val Asp Phe Glu Ser
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Ser Glu Asp Asp Asp Asp Asp Pro Phe Met Asn Thr Ser Ser Leu Arg
690 695 700
Arg Asn Arg Arg
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<210> 3
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<212> PRT
<213> Homo sapiens

<220>
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Phe Met Glu Lys Asp Ala Ala Arg Gly Asn Asp Thr Phe Val Thr Leu
20 25 30
Asp Glu Ile Leu Arg Leu Ala Gln Glu Asn Glu Val Asp Phe Ile Leu
35 40 45
Leu Gly Gly Asp Leu Phe His Glu Asn Lys Pro Ser Arg Lys Thr Leu
50 55 60
His Thr Cys Leu Glu Leu Leu Arg Lys Tyr Cys Met Gly Asp Arg Pro
65 70 75 80
Val Gln Phe Glu Ile Leu Ser Asp Gln Ser Val Asn Phe Gly Phe Ser
85 90 95
Lys Phe Pro Trp Val Asn Tyr Gln Asp Gly Asn Leu Asn Ile Ser Ile
100 105 110
Pro Val Phe Ser Ile His Gly Asn His Asp Asp Pro Thr Gly Ala Asp
115 120 125
Ala Leu Cys Ala Leu Asp Ile Leu Ser Cys Ala Gly Phe Val Asn His
130 135 140
Phe Gly Arg Ser Met Ser Val Glu Lys Ile Asp Ile Ser Pro Val Leu
145 150 155 160
Leu Gln Lys Gly Ser Thr Lys Ile Ala Leu Tyr Gly Leu Gly Ser Ile
165 170 175
Pro Asp Glu Arg Leu Tyr Arg Met Phe Val Asn Lys Lys Val Thr Met
180 185 190
Leu Arg Pro Lys Glu Asp Glu Asn Ser Trp Phe Asn Leu Phe Val Ile
195 200 205
His Gln Asn Arg Ser Lys His Gly Ser Thr Asn Phe Ile Pro Glu Gln
210 215 220
Phe Leu Asp Asp Phe Ile Asp Leu Val Ile Trp Gly His Glu His Glu
225 230 235 240
Cys Lys Ile Ala Pro Thr Lys Asn Glu Gln Gln Leu Phe Tyr Ile Ser
245 250 255
Gln Pro Gly Ser Ser Val Val Thr Ser Leu Ser Pro Gly Glu Ala Val
260 265 270
Lys Lys His Val Gly Leu Leu Arg Ile Lys Gly Arg Lys Met Asn Met
275 280 285
His Lys Ile Pro Leu His Thr Val Arg Gln Phe
290 295

<210> 4
<211> 300
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<223> yeast MRE11 amino acids 5-304

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His Glu Val Met Met Leu Ala Lys Asn Asn Asn Val Asp Met Val Val
            35                  40                  45
Gln Ser Gly Asp Leu Phe His Val Asn Lys Pro Ser Lys Lys Ser Leu
        50                  55                  60
Tyr Gln Val Leu Lys Thr Leu Arg Leu Cys Cys Met Gly Asp Lys Pro
 65                  70                  75                  80
Cys Glu Leu Glu Leu Leu Ser Asp Pro Ser Gln Val Phe His Tyr Asp
                85                  90                  95
Glu Phe Thr Asn Val Asn Tyr Glu Asp Pro Asn Phe Asn Ile Ser Ile
            100                 105                 110
Pro Val Phe Gly Ile Ser Gly Asn His Asp Asp Ala Ser Gly Asp Ser
        115                 120                 125
Leu Leu Cys Pro Met Asp Ile Leu His Ala Thr Gly Leu Ile Asn His
    130                 135                 140
Phe Gly Lys Val Ile Glu Ser Asp Lys Ile Lys Val Val Pro Leu Leu
145                 150                 155                 160
Phe Gln Lys Gly Ser Thr Lys Leu Ala Leu Tyr Gly Leu Ala Ala Val
                165                 170                 175
Arg Asp Glu Arg Leu Phe Arg Thr Phe Lys Asp Gly Gly Val Thr Phe
            180                 185                 190
Glu Val Pro Thr Met Arg Glu Gly Glu Trp Phe Asn Leu Met Cys Val
        195                 200                 205
His Gln Asn His Thr Gly His Thr Asn Thr Ala Phe Leu Pro Glu Gln
    210                 215                 220
Phe Leu Pro Asp Phe Leu Asp Met Val Ile Trp Gly His Glu His Glu
225                 230                 235                 240
Cys Ile Pro Asn Leu Val His Asn Pro Ile Lys Asn Phe Asp Val Leu
                245                 250                 255
Gln Pro Gly Ser Ser Val Ala Thr Ser Leu Cys Glu Ala Glu Ala Gln
            260                 265                 270
Pro Lys Tyr Val Phe Ile Leu Asp Ile Lys Tyr Gly Glu Ala Pro Lys
        275                 280                 285
Met Thr Pro Ile Pro Leu Glu Thr Ile Arg Thr Phe
    290                 295                 300
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<210> 5
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<220>
<223> Description of Artificial Sequence:consensus MRE11 peptide

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<210> 6
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus MRE11 peptide

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<222> (5)
<223> Xaa = Arg or Lys

<220>
<221> MOD_RES
<222> (7)
<223> Xaa = Thr or Ser

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<221> MOD_RES
<222> (9)
<223> Xaa = His or Tyr

<400> 6
Asn Lys Pro Ser Xaa Lys Xaa Leu Xaa
1 5

<210> 7
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus MRE11 peptide

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<223> Xaa = Arg or Lys

<400> 7
Cys Met Gly Asp Xaa Pro
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<210> 8
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus MRE11 peptide

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<223> Xaa = Ile or Leu

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<210> 9
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus MRE11
peptide

<400> 9
Val Asn Tyr Glx Asp
1 5

<210> 10
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus MRE11
peptide

<400> 10
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<210> 11
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus MRE11
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<400> 11
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<210> 12
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
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peptide

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<223> Xaa = Val or Ile

<220>
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<223> Xaa = Arg or Lys

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<210> 13
<211> 12
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus MRE11 peptide

<220>
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<223> Xaa = Ile or Leu

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<210> 14
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus MRE11 peptide

<220>
<221> MOD_RES
<222> (5)
<223> Xaa = Tyr or Phe

<400> 14
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<210> 15
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<212> PRT
<213> Artificial Sequence

<220>
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<210> 16
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus MRE11
peptide

<220>
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<400> 16
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1 5

<210> 17
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<212> PRT
<213> Artificial Sequence

<220>
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peptide

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<222> (3)
<223> Xaa = Ile or Leu

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<221> MOD_RES
<222> (5)
<223> Xaa = Leu or Met

<400> 17
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<210> 18
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus MRE11
peptide

<400> 18
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1 5

<210> 19
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide
duplex substrate for MRE11 plate-based assay

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<222> (1)
<223> n = c modified by biotin

<220>
<221> modified_base
<222> (27)
<223> n = 5-bromo-2'-deoxyuridine

<220>
<221> modified_base
<222> (40)
<223> n = 5-bromo-2'-deoxyuridine

<400> 19
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<210> 20
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide
duplex substrate for MRE11 plate-based assay

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<210> 21
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<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:poly Gly
flexible linker

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<222> (6)..(200)
<223> Gly residues from position 6 to 200 may be present
or absent

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20 25 30
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
35 40 45
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
50 55 60
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
65 70 75 80
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
85 90 95

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Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
                100                 105                 110
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
        115                 120                 125
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
    130                 135                 140
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
145                 150                 155                 160
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
                165                 170                 175
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
            180                 185                 190
Gly Gly Gly Gly Gly Gly Gly Gly
        195                 200
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